



SEQUENCE LISTING

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<120> Method for Studying Protein Interactions in Vivo

<130> 11785-3

<140> US 09/786377

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<150> US 60/099,068

<151> 1998-09-03

<150> PCT/US99/20207

<151> 1999-09-02

<160> 10

<170> PatentIn version 3.0

<210> 1

<211> 918

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(719)

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ctg ctc gct gcc agc cca gga ggc gcc ttg gcg cgg tgc cca ggc tgc 95
Leu Leu Ala Ala Ser Pro Gly Gly Ala Leu Ala Arg Cys Pro Gly Cys
20 25 30

ggc caa ggg gtg cag gcg ggt tgt cca ggg ggc tgc gtg gag gag gag 143
Gly Gln Gly Val Gln Ala Gly Cys Pro Gly Gly Cys Val Glu Glu Glu
35 40 45

gat ggg ggg tcg cca gcc gag ggc tgc gcg gaa gct gag ggc tgt ctc 191
Asp Gly Gly Ser Pro Ala Glu Gly Cys Ala Glu Ala Glu Gly Cys Leu
50 55 60

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agg agg gag ggg cag gag tgc ggg gtc tac acc cct aac tgc gcc cca 239
 Arg Arg Glu Gly Gln Glu Cys Gly Val Tyr Thr Pro Asn Cys Ala Pro
 65 70 75

gga ctg cag tgc cat ccg ccc aag gac gac gag gcg cct ttg cgg gcg 287
 Gly Leu Gln Cys His Pro Pro Lys Asp Asp Glu Ala Pro Leu Arg Ala
 80 85 90 95

ctg ctg ctc ggc cga ggc cgc tgc ctt ccg gcc cgc gcg cct gct gtt 335
 Leu Leu Leu Gly Arg Gly Arg Cys Leu Pro Ala Arg Ala Pro Ala Val
 100 105 110

gca gag gag aat cct aag gag agt aaa ccc caa gca ggc act gcc cgc 383
 Ala Glu Glu Asn Pro Lys Glu Ser Lys Pro Gln Ala Gly Thr Ala Arg
 115 120 125

cca cag gat gtg aac cgc aga gac caa cag agg aat cca ggc acc tct 431
 Pro Gln Asp Val Asn Arg Arg Asp Gln Gln Arg Asn Pro Gly Thr Ser
 130 135 140

acc acg ccc tcc cag ccc aat tct gcg ggt gtc caa gac act gag atg 479
 Thr Thr Pro Ser Gln Pro Asn Ser Ala Gly Val Gln Asp Thr Glu Met
 145 150 155

ggc cca tgc cgt aga cat ctg gac tca gtg ctg cag caa ctc cag act 527
 Gly Pro Cys Arg Arg His Leu Asp Ser Val Leu Gln Gln Leu Gln Thr
 160 165 170 175

gag gtc tac cga ggg gct caa aca ctc tac gtg ccc aat tgt gac cat 575
 Glu Val Tyr Arg Gly Ala Gln Thr Leu Tyr Val Pro Asn Cys Asp His
 180 185 190

cga ggc ttc tac cgg aag cgg cag tgc cgc tcc tcc cag ggg cag cgc 623
 Arg Gly Phe Tyr Arg Lys Arg Gln Cys Arg Ser Ser Gln Gly Gln Arg
 195 200 205

cga ggt ccc tgc tgg tgt gtg gat cgg atg ggc aag tcc ctg cca ggg 671
 Arg Gly Pro Cys Trp Cys Val Asp Arg Met Gly Lys Ser Leu Pro Gly
 210 215 220

tct cca gat ggc aat gga agc tcc tcc tgc ccc act ggg agt agc ggc 719
 Ser Pro Asp Gly Asn Gly Ser Ser Ser Cys Pro Thr Gly Ser Ser Gly
 225 230 235

taaagctggg ggatagaggg gctgcagggc cactggaagg aacatggagc tgtcatcact
 779

caacaaaaaaaaa ccgaggccct caatccacct tcaggccccg ccccatgggc ccctcaccgc
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35 40 45

Gly Gly Ser Pro Ala Glu Gly Cys Ala Glu Ala Glu Gly Cys Leu Arg
50 55 60

Arg Glu Gly Gln Glu Cys Gly Val Tyr Thr Pro Asn Cys Ala Pro Gly
65 70 75 80

Leu Gln Cys His Pro Pro Lys Asp Asp Glu Ala Pro Leu Arg Ala Leu
85 90 95

Leu Leu Gly Arg Gly Arg Cys Leu Pro Ala Arg Ala Pro Ala Val Ala
100 105 110

Glu Glu Asn Pro Lys Glu Ser Lys Pro Gln Ala Gly Thr Ala Arg Pro
115 120 125

Gln Asp Val Asn Arg Arg Asp Gln Gln Arg Asn Pro Gly Thr Ser Thr
130 135 140

Thr Pro Ser Gln Pro Asn Ser Ala Gly Val Gln Asp Thr Glu Met Gly
145 150 155 160

Pro Cys Arg Arg His Leu Asp Ser Val Leu Gln Gln Leu Gln Thr Glu
165 170 175

Val Tyr Arg Gly Ala Gln Thr Leu Tyr Val Pro Asn Cys Asp His Arg
180 185 190

Gly Phe Tyr Arg Lys Arg Gln Cys Arg Ser Ser Gln Gly Gln Arg Arg
195 200 205

Gly Pro Cys Trp Cys Val Asp Arg Met Gly Lys Ser Leu Pro Gly Ser
210 215 220

Pro Asp Gly Asn Gly Ser Ser Ser Cys Pro Thr Gly Ser Ser Gly
225 230 235

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<212> DNA

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<222> (10)..(945)

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Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu
15 20 25 30

gat tca ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct 147
Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala
35 40 45

gtt att ttt tta cat ggt aac gac gcg gcc tct tct tat tta tgg cga cat 195
Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His
50 55 60

gtt gtg cca cat att gag cca gta gcg cgg tgg att ata cca gat ctt 243
Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu
65 70 75

att ggt atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta 291
Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu
80 85 90

ctt gat cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta 339
Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu
95 100 105 110

cca aag aag atc att ttt gtc ggc cat gat tgg ggt gct tgg gca 387
Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala
115 120 125

ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac 435
Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His
130 135 140

gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat 483
Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp
145 150 155

att gaa gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg 531
Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met
160 165 170

gtt ttg gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc	579
Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile	
175 180 185 190	
atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc	627
Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe	
195 200 205	
aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa	675
Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu	
210 215 220	
atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg	723
Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg	
225 230 235	
aat tat aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt	771
Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe	
240 245 250	
att gaa tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc	819
Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala	
255 260 265 270	
aag aag ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt	867
Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe	
275 280 285	
tcg caa gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc	915
Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe	
290 295 300	
gtt gag cga gtt ctc aaa aat gaa caa taa ttacttttgt tttttattta	965
Val Glu Arg Val Leu Lys Asn Glu Gln	
305 310	
cattttccc gggtaata atataatgt cattttcaac aattttattt taactgaata	1025
tttcacaggg aacattcata tatgttgatt aat tagctc gaactttact ctgtcatatc	1085
attttggaat attacctctt tcaatgaaac tttataaaca gtggttcaat taattaatat	1145
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35 40 45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
50 55 60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
65 70 75 80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
85 90 95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
100 105 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
115 120 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
130 135 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145 150 155 160

Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
165 170 175

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
180 185 190

Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
195 200 205

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
210 215 220

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225 230 235 240

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
245 250 255

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
260 265 270

Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
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Arg Val Leu Lys Asn Glu Gln
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<213> Homo sapiens

<220>
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<222> (1)..(543)

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Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu	
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tgc ggc ggg gag ctg gtg gac acc ctc cag ttc gtc tgt ggg gac cgc	144
Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg	
35 40 45	
ggc ttc tac ttc agc agg ccc gca agc cgt gtg agc cgt cgc agc cgt	192
Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg	
50 55 60	
ggc atc gtt gag gag tgc tgt ttc cgc agc tgt gac ctg gcc ctc ctg	240
Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu	
65 70 75 80	
gag acg tac tgt gct acc ccc gcc aag tcc gag agg gac gtg tcg acc	288
Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr	
85 90 95	
cct ccg acc gtg ctt ccg gac aac ttc ccc aga tac ccc gtg ggc aag	336
Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys	
100 105 110	
ttc ttc caa tat gac acc tgg aag cag tcc acc cag cgc ctg cgc agg	384
Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg	
115 120 125	
ggc ctg cct gcc ctc ctg cgt gcc cgc cgg ggt cac gtg ctc gcc aag	432
Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys	
130 135 140	
gag ctc gag gcg ttc agg gag gcc aaa cgt cac cgt ccc ctg att gct	480
Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala	
145 150 155 160	

ctc ccc acc caa gac ccc gcc cac ggg ggc gcc ccc cca gag atg gcc 528
Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
165 170 175

agc aat cgg aag tga 543
Ser Asn Arg Lys
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Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
35 40 45

Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
50 55 60

Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu
65 70 75 80

Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
85 90 95

Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
100 105 110

Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
115 120 125

Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
130 135 140

Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
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Ser Asn Arg Lys
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gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	tct	gtc	agc	gga	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
20			25						30							
ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	ctg	aaa	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
35			40							45						
acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	ctg	gtc	act	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
50			55					60								
tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	gac	cat	atg	aag	cag	240
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
65			70					75					80			
cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	tat	gtg	cag	gag	aga	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90				95				
acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	acc	cgc	gct	gaa	gtc	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100				105			110					
aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	gag	ctg	aag	ggc	att	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
				115				120			125					
gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	aag	ctg	gaa	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
				130				135			140					
tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	aag	caa	aag	aat	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
				145				150			155		160			
atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	gag	gat	gga	tcc	gtg	528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	

165

170

175

cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct 576
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct 624
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg 672
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 717
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly

145

150

155

160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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<212> DNA

<213> Homo sapiens

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<222> (1)..(333)

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 1 5 10 15

tgg gga cct gac cca gca gcc ttt gtg aac caa cac ctg tgc ggc 96
 Trp Gly Pro Asp Pro Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30

tca cac ctg gtg gaa gct ctc tac cta gtg tgc ggg gaa cga ggc ttc 144
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45

ttc tac aca ccc aag acc cgc cgg gag gca gag gac ctg cag gtg ggg 192
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60

cag gtg gag ctg ggc ggg ggc cct ggt gca ggc agc ctg cag ccc ttg 240
 Gln Val Glu Leu Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80

gcc ctg gag ggg tcc ctg cag aag cgt ggc att gtg gaa caa tgc tgt 288
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95

acc agc atc tgc tcc ctc tac cag ctg gag aac tac tgc aac tag 333
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100

105

110

<210> 10
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Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
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20 25 30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
35 40 45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
50 55 60

Gln Val Glu Leu Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65 70 75 80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
85 90 95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
100 105 110